- 1 -

SEQUENCE LISTING

<110> Agriculture Victoria Services Pty Ltd AND Pig Research and Development Corporation AND Pfizer Products Inc.

<120> Novel lawsonia spp. gene and uses therefor V

<130> p:\oper\mro\lawson-5.pct

<140>

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<150> US 60/133,989

<151> 1999-05-12

<160> 5

<170> PatentIn Ver. 2.0

<210> 1

<211> 180

<212> PRT

<213> Lawsonia intracellularis

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Met Lys Ile Lys Leu Phe Phe Val Thr Ser Ile Val Thr Ile Ser Leu
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Leu Thr Ser Ile Thr Ser Val Val Leu Ala Cys Ser Val Thr Ser Glu
                20   25   30

Val His Met Ile Asp Asp Asn Gly Ile Lys Gln Ser Ile Gly Thr Val
            35   40   45

Thr Phe Thr Asp Thr Asp Lys Gly Leu Gln Ile Lys Thr Asp Leu Lys
        50   55   60

Gly Leu Pro Ala Gly Glu His Gly Phe His Ile His Glu Gly Gly Ser
65   70   75   80

Cys Gly Pro Ala Glu His Asp Gly His Leu Thr Ala Gly Leu Gln Ala
                85   90   95

His Gly His Tyr Asp Pro Asp Lys Thr Gly Lys His Glu Gly Pro Leu
                100   105   110

Gly Asn Gly His Lys Gly Asp Leu Pro Arg Leu Val Val Lys Ala Asp
                115   120   125

Gly Ile Ala Lys Glu Thr Leu Leu Ala Pro Arg Leu Thr Val Lys Glu
            130   135   140

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Ile Lys Gly Arg Thr Val Met Ile His Ala Gly Gly Asp Asn Tyr Ser
145             150             155             160

Asp Lys Pro Leu Pro Leu Gly Gly Gly Gly Ala Arg Ile Ala Cys Gly
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Val Ile Pro Asn
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  1               5              10              15

tta act agt att act agt gta gta tta gca tgt tct gtt act tca gaa    96
Leu Thr Ser Ile Thr Ser Val Val Leu Ala Cys Ser Val Thr Ser Glu
            20              25              30

gtc cat atg att gat gac aat gga ata aaa cag agt ata ggc aca gta   144
Val His Met Ile Asp Asp Asn Gly Ile Lys Gln Ser Ile Gly Thr Val
        35              40              45

act ttt act gat aca gat aaa ggt cta caa ata aaa act gat ctt aaa   192
Thr Phe Thr Asp Thr Asp Lys Gly Leu Gln Ile Lys Thr Asp Leu Lys
    50              55              60

ggc ctt cct gca gga gaa cat ggt ttt cat atc cat gaa gga gga tca   240
Gly Leu Pro Ala Gly Glu His Gly Phe His Ile His Glu Gly Gly Ser
 65              70              75              80

tgt gga cct gct gag cat gat gga cat cta aca gct gga ctc caa gct   288
Cys Gly Pro Ala Glu His Asp Gly His Leu Thr Ala Gly Leu Gln Ala
                85              90              95

cat ggt cat tat gat cct gac aaa aca gga aaa cat gaa gga cct ctt   336
His Gly His Tyr Asp Pro Asp Lys Thr Gly Lys His Glu Gly Pro Leu
            100             105             110
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ggt aat gga cac aag gga gac tta cct aga ctt gta gtt aaa gct gat    384
Gly Asn Gly His Lys Gly Asp Leu Pro Arg Leu Val Val Lys Ala Asp
        115                 120                 125

gga ata gca aaa gaa aca ctc tta gct cca aga tta aca gtt aaa gaa    432
Gly Ile Ala Lys Glu Thr Leu Leu Ala Pro Arg Leu Thr Val Lys Glu
        130                 135                 140

att aag ggt cgt aca gtt atg atc cat gct ggt ggt gat aac tat tca    480
Ile Lys Gly Arg Thr Val Met Ile His Ala Gly Gly Asp Asn Tyr Ser
145                 150                 155                 160

gat aaa cct ctt cct ctt ggc ggt ggt ggt gct cgt ata gct tgt ggt    528
Asp Lys Pro Leu Pro Leu Gly Gly Gly Gly Ala Arg Ile Ala Cys Gly
                165                 170                 175

gtt ata cca aac tag                                                543
Val Ile Pro Asn
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